IN THE U.S. PATENT AND TRADEMARK OFFICE

Applicant:

Klaus K. NIELSEN et al.

Conf.:

5659

Appl. No.:

10/507,355

Art Unit:

N/A

Filed:

June 9, 2005

Examiner:

Not Yet Assigned

For:

METHOD FOR REPRESSING FLOWERING IN A PLANT

DECLARATION SUBMITTED UNDER 37 C.F.R. § 1.132

Honorable Commissioner Of Patents and Trademarks P.O. Box 1450 Alexandria, VA 22313-1450

April 30, 2008

Sir:

I, Dr. Ingo Peter Lenk of the Research Department, DLF-TRIFOLIUM A/S, Denmark, do hereby declare the following:

I have attached a copy of my curriculum vitae to this Declaration.

I am employed as research scientist at the Research Department, DLF-TRIFOLIUM A/S and have worked in the field of flowering control in plants for more than 6 years.

I am familiar with the above referenced patent application, (the Nielsen et al. application), and the area of science dealing with the control of flowering in plants and its genetic basis. I am also well versed in the molecular biology of plants, methods for transforming plants and the analysis of the morphology of flowering organs of plants in its diverse stages of development.

I have read and understand the subject matter of the Office Action dated January 2, 2008.

The following comments are offered in support of the patentability of the instant invention.

The Examiner criticizes the application's support for written description and enablement based on the breadth of the sequence definition recited in claim 1 and states that the specification lacks sufficient information on the structure common to the polynucleotides covered by the claims.

In reply, I state that the Examiner's criticism is not appropriate or valid with respect to the amended sequence definition. The amended claim 1 defines the sequence (i) to show a sequence identity of at least 83% to the specific nucleotide sequences defined in sections (a) and (b) of claim 1; (ii) by the fact that the encoded polypeptide has LpTFL1-like activity; and (iii) by the fact that the encoded polypeptide comprises the amino acid sequence YESP(K/R). In support, I refer to the attached Table (Annex I) that I have prepared. This Table lists genes homologous to LpTFL1 that are retrievable from public databases and indicates their sequence identities to LpTFL1 (both on the nucleotide level and the amino acid level). All of the genes in the Table that have an identity of at least 83% on the nucleotide level encode an amino acid sequence having the motif YESP(K/R). From my experience, it is reasonable to believe that one of skill in the art would recognize that these sequences will be useful for reducing or preventing flowering in plants by expressing them therein, as was shown in the patent application for LpTFL1.

Additionally, in my opinion, one of skill in the art reading the Nielsen et al. application would recognize that as of the date of filing, applicants were in possession of

the Invention defined as sequences showing 83% Identity to the specific nucleotide sequences in sections (a) and (b) of clalm 1, which encode a polypeptide having LpTFL1-like activity, which also have a YESP(K/R) motif. See for example the specification at page 6, line 3 (describing a sequence with 83% Identity to sequences in claim 1(a) and (b)) and page 12, paragraph 2 (describing the importance of the YESP(K/R) region to flowering). This is supported by the present data found in the Table (Annex 1) in combination with the specification because the species in the table conform to the elements of the claimed genus: (i) the genes presented by the table have at least 83% Identity with the sequences of those in claim 1(a) and (b), (ii) the sequences all have a YESP(K/R) region, and (iii) the specification discloses that homologues with 83% sequence identity to LpTFL-1 with a YESP(K/R) region could reasonably be expected to suppress flowering. (See Table (Annex 1) and the Specification of the Nielsen et al. application at page 12, paragraph 2, and page 31, beginning at line 7).

In forming my opinion, stated above, I have considered:

- a. The actual working examples described in the Nielsen et al application.
- b. The disclosed structure of the claimed nucleotide sequence.
- The disclosure of the YESP(K/R) motif for the claimed sequences and its relation to flowering.
- d. The method for making the present invention, as well as the predictability and level of skill in the art.

The undersigned hereby declares that all statements made herein based upon knowledge are true, and that all statements made based upon information and belief are believed to be true; and further, that these statements were made with the knowledge

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that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

DATED: 30.4.200 8

Dr. Ingo Peter Lenk

DESCR	species An	Amino acid II Nucleotide ID	eotide ID	motif
AF316419_1terminal flower 1-like protein	Lolium perenne	100,0%	100,0%	YESPK
terminal flower 1-like protein	Hordeum vulgare subsp. vulgare	88.8%	90.3%	YESPK
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CEN/TFL1-like GTP-associated binding protein	Lotus japonicus	80,4%	73,1%	YEIPK
BNTFL1-2	Brassica napus	80,4%	73,0%	YELPK
TFL1-like protein	Eriobotrya japonica	80,4%	72,7%	YEMPR
ZCN4 protein	Zea mays	%8'8%	72,0%	YESPK
BOTFL1-1	Brassica oleracea	80,4%	71,8%	YELPK
ZCN5	Zea mays	80,4%	71,4%	YESPK
ZCN5 protein	Zea mays	80,4%	71,4%	YESPK
late-flowering	Pisum satívum	80,4%	%6'02	YEKPK

DEFINITION	NT_GI	PROT GI
Lolium perenne terminal flower 1-like protein (TFL1) mRNA, complete	11139707	11139708
Hordeum vulgare subsp. vulgare terminal flower 1-like protein	107857326	107857326 107857327
Orza setive (electrice cultivar-graup. 38.1 golistzőjő (obil) görzősőső,	(A) (表现是自己的	11,5418,42119
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Lotus japonicus CEN/TFL1-like GTP-associated binding protein (cen1)	37575146	37575147
Brassica napus BNTFL1-2 gene, complete cds.	3650420	3650421
Eriobotrya japonica EjTFL1-2 mRNA for TFL1-like protein, complete	42491325	42491326
Zea mays ZCN4 protein (ZCN4), mRNA.	163838715	163838716
Brassica oleracea BOTFL1-1 gene, partial cds.	3650428	3650429
Zea mays ZCN5 (ZCN5) gene, complete cds.	160213483	160213484
Zea mays ZCN5 protein (ZCN5), mRNA.	163838717	163838718
Pisum sativum late-flowering (LF) gene, complete cds.	33518653	33518654

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Curriculum vitae Ingo Lenk

Ingo Lenk, PhD, Research Scientist DLF-TRIFOLIUM A/S, Research Division, 31 Højerupvej, 4660 Store Heddinge, Denmark Phone +45 7233 0434, Fax +45 5650 3524, E-mail il@dlf.dk

Present employment: Research Scientist, DLF-Trifolium A/S, Denmark (since 2003)

Academic degrees:

Dipl. Biologist (M.Sc.), Department for Genetics, University of Bielefeld Dr. rer. nat. (Ph.D.) in Botany and Genetics, University of Göttingen

Previous employments: Post-doctoral Scientist, DLF-Trifolium A/S, Denmark (2001-2003)

Scientific and administrative activities:

- Development of ryegrass allele-specific (GRASP) markers

- Member of the expert group for implementation of storage protein gel electrophoresis in ryegrass at the Bundessortenamt, Germany

- Establish *Brachypodium distachyon* as model plant (incl. development of transformation protocols, adaptation of laboratory and phenotyping protocols for transgene studies)

- Dissection of floral transition mechanisms in temperate grasses

- Pathogen related stress signalling in plants

- Chemically inducible synthetic promoters

Fellowships: Marie-Curie Industry Host Fellowship (2001 – 2003)

Publications:

Păcurar Dl, Thordal-Christensen H, Nielsen KK, Lenk I

A high-throughput Agrobacterium-mediated transformation system for the grass model species Brachypodium distachyon L.

Transgenic Res. 2007 Dec 7 [Epub ahead of print]

Ciannamea S, Jensen CS, Agerskov H, Petersen K, Lenk I, Didion T, Immink RGH, Angenent GC, Nielsen KK

A new member of the LIR gene family from perennial ryegrass is cold-responsive, and promotes vegetative growth in Arabidopsis

Plant Science 2007; 172 (2) 221-227

Olsen P, Lenk I, Jensen CS, Petersen K, Andersen CH, Didion T, Nielsen KK Analysis of two heterologous flowering genes in *Brachypodium distachyon* demonstrates its potential as a grass model plant

Plant Science 2006; 170 (5) 1020-1025

Kegler C, Lenk I, Krawczyk S, Scholz R, Gatz C Functional characterization of tobacco transcription factor TGA2.1. Plant Mol Biol. 2004; 55:153-64.

Bohner S, Lenk I, Rieping M, Herold M, Gatz C Technical advance: transcriptional activator TGV mediates dexamethasone-inducible and tetracycline-inactivatable gene expression Plant J. 1999 Jul; 19(1):87-95.

Thiele A, Herold M, Lenk I, Quail PH, Gatz C Heterologous expression of Arabidopsis phytochrome B in transgenic potato influences photosynthetic performance and tuber development. Plant Physiol. 1999 May; 120(1):73-82.

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Promoters that respond to chemical inducers
Trends in Plant Science 1998 September; 3(9):352-358

Patents:

Nielsen KK, Andersen CH, Folling M, Gao C, Lenk I, Didion T, Jensen CS, Petersen K, Storgaard M Means and Methods for Controlling Flowering in Plants. WO/2006/005520

Nielsen KK, Andersen CH, Lenk I, Petersen K, Didion T Tissue specific promoters from plants. WO/2004/035797

Oral Presentations:

Ingo Lenk, Daniel Pacurar, Pernille Christiansen, Hans Thordal-Christensen, Klaus K. Nielsen: Brachypodium distachyon as a model for temperate grasses and cereals Invited Oral Presentation at the COST Action 851 Workshop, Copenhagen 2005

Ingo Lenk, Pernille Christiansen, Marianne Folling, Caixia Gao, Klaus K. Nielsen: Brachypodium distachyon as a test bed for monocot genetics

Oral Presentation at the 7 International Congress of Plant Molecular Biology, Barcelona 2003